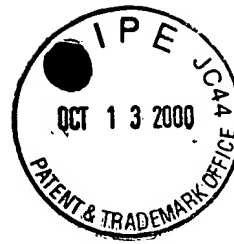


SEQUENCE LISTING



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(1) GENERAL INFORMATION:

(i) APPLICANT: Little, Andrew  
Lamparski, Henry  
Schuur, Eric  
Henderson, Daniel

(ii) TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS  
EXPRESSING ALPHA-FETOPROTEIN AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER  
(B) STREET: 755 PAGE MILL ROAD  
(C) CITY: PALO ALTO  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/509,591  
(B) FILING DATE: 02-JUN-2000  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US98/04084  
(B) FILING DATE: 03-MAR-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: POLIZZI, CATHERINE M.  
(B) REGISTRATION NUMBER: 40,130  
(C) REFERENCE/DOCKET NUMBER: 348022000420

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(C) TELEX: 706141 MRSNFOERS SFO

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCATTGCTGT GAACTCTGTA CTTAGGACTA AACTTTGAGC AATAACACAC ATAGATTGAG	60
GATTGTTTGC TGTTAGCATA CAAACTCTGG TTCAAAGCTC CTCTTTATTG CTTGTCTTGG	120
AAAATTTGCT GTTCTTCATG GTTTCTCTTT TCACTGCTAT CTATTTTCT CAACCACTCA	180
CATGGCTACA ATAAGTGTCT GCAAGCTTAT GATTCCCAA TATCTATCTC TAGCCTCAAT	240
CTTGTTCCAG AAGATAAAAA GTAGTATTCA AATGCACATC AACGTCTCCA CTTGGAGGGC	300
TTAAAGACGT TTCAACATAC AAACCGGGGA GTTTTGCCTG GAATGTTTCC TAAAATGTGT	360
CCTGTAGCAC ATAGGGTCCT CTTGTTCCCT AAAATCTAAT TACTTTTAGC CCAGTGCTCA	420
TCCCACCTAT GGGGAGATGA GAGTGAAAAG GGAGCCTGAT TAATAATTAC ACTAAGTCAA	480
TAGGCATAGA GCCAGGACTG TTTGGGTAAA CTGGTCACTT TATCTTAAAC TAAATATATC	540
CAAACTGAA CATGTACTTA GTTACTAAGT CTTTGACTTT ATCTCATTCA TACCACTCAG	600
CTTTATCCAG GCCACTTATG AGCTCTGTGT CCTTGAACAT AAAATACAAA TAACCGCTAT	660
GCTGTTAATT ATTGGCAAAT GTCCCATTTT CAACCTAAGG AAATACCATA AAGTAACAGA	720
TATACCAACA AAAGGTTACT AGTTAACAGG CATTGCCTGA AAAGAGTATA AAAGAATTC	780
AGCATGATTT TCCATATTGT GCTTCCACCA CTGCCAATAA CA	822

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCTTAG AAATATGGGG GTAGGGGTGG TGGTGTAAT TCTGTTTCA CCCCATAGGT	60
GAGATAAGCA TTGGGTTAAA TGTGCTTTCA CACACACATC ACATTCATA AGAATTAAGG	120
AACAGACTAT GGGCTGGAGG ACTTTGAGGA TGTCTGTCTC ATAACACTTG GGTGTATCT	180
GTTCTATGGG GCTTGTTTTA AGCTTGCAA CTTGCAACAG GGTTCCTGA CTTTCTCCCC	240
AAGCCCAAGG TACTGTCCTC TTTTCATATC TGTTTTGGGG CCTCTGGGGC TTGAATATCT	300
GAGAAAATAT AAACATTTCA ATAATGTTCT GTGGTGAGAT GAGTATGAGA GATGTGTCAT	360
TCATTTGTAT CAATGAATGA ATGAGGACAA TTAGTGTATA AATCCTTAGT ACAACAATCT	420
GAGGGTAGGG GTGGTACTAT TCAATTTCTA TTTATAAAGA TACTTATTC TATTTATTTA	480
TGCTTGTGAC AAATGTTTTG TTCGGGACCA CAGGAATCAC AAAGATGAGT CTTTGAATTT	540

AAGAAGTTAA TGGTCCAGGA ATAATTACAT AGCTTACAAA TGA	600
CTATATGAT ATACCATCAA	
ACAAGAGGTT CCATGAGAAA ATAATCTGAA AGGTTTAATA AGTTGT	660
CATAA GGTGAGAGGG	
CTCTTCTCTA GCTAGAGACT AATCAGAAAT ACATTCAGGG ATAATTATTT	720
GAATAGACCT	
TAAGGGTTGG GTACATTTTG TTCAAGCATT GATGGAGAAG GAGAGTGAAT	780
ATTTGAAAAC	
ATTTTCAACT AACCAACCAC CCAATCCAAC AAACAAAAAA TGAAAAGAAT	840
CTCAGAAACA	
GTGAGATAAG AGAAGGAATT TTCTCACAAC CCACACGTAT AGCTCAACTG	900
CTCTGAAGAA	
GTATATATCT AATATTTAAC ACTAACATCA TGCTAATAAT GATAATAATT	960
ACTGTCATTT	
TTTAATGTCT ATAAGTACCA GGCATTTAGA AGATATTATT CCATTTATAT	1020
ATCAAAATAA	
ACTTGAGGGG ATAGATCATT TTCATGATAT ATGAGAAAAA TTAAAAACAG	1080
ATTGAATTAT	
TTGCCTGTCA TACAGCTAAT AATTGACCAT AAGACAATTA GATTTAAATT	1140
AGTTTTGAAT	
CTTTCTAATA CCAAAGTTCA GTTTACTGTT CCATGTTGCT TCTGAGTGGC	1200
TTCACAGACT	
TATGAAAAAG TAAACGGAAT CAGAATTACA TCAATGCAAA AGCATTGCTG	1260
TGAACTCTGT	
ACTTAGGACT AAACTTTGAG CAATAACACA CATAGATTGA GGATTGTTTG	1320
CTGTTAGCAT	
ACAAACTCTG GTTCAAAGCT CCTCTTTATT GCTTGTCTTG GAAAATTTGC	1380
TGTTCTTCAT	
GGTTTCTCTT TTCACTGCTA TCTATTTTTC TCAACCACTC ACATGGCTAC	1440
AATAACTGTC	
TGCAAGCTTA TGATTCCCAA ATATCTATCT CTAGCCTCAA TCTTGTCCA	1500
GAAGATAAAA	
AGTAGTATTC AAATGCACAT CAACGTCTCC ACTTGGAGGG CTTAAAGACG	1560
TTCAACATA	
CAAACCGGGG AGTTTTGCCT GGAATGTTTC CTAAAATGTG TCCTGTAGCA	1620
CATAGGGTCC	
TCTTGTTTCT TAAATCTAA TTA	1680
CTTTTAG CCCAGTGCTC ATCCACCTA TGGGGAGATG	
AGAGTGAAAA GGGAGCCTGA TTAATAATTA CACTAAGTCA ATAGGCATAG	1740
AGCCAGGACT	
GTTTGGGTAA ACTGGTCACT TTATCTTAAA CTAAATATAT CCAAAACTGA	1800
ACATGTACTT	
AGTTACTAAG TCTTTGACTT TATCTCATTC ATACCACTCA GCTTTATCCA	1860
GGCCACTTAT	
TTGACAGTAT TATTGCGAAA ACTTCCTAAC TGGTCTCCTT ATCATAGTCT	1920
TATCCCCTTT	
TGAAACAAAA GAGACAGTTT CAAAATACAA ATATGATTTT TATTAGCTCC	1980
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CTATAATAGT CCCAGAAGGA GTTATAAACT CCATTTAAAA AGTCTTTGAG	2040
ATGTGGCCCT	
TGCCAACTTT GCCAGGAATT CCCAATATCT AGTATTTTCT ACTATTAAAC	2100
TTTGTGCCTC	
TTCAAACTG CATTTTCTCT CATTCCTTAA GTGTGCATTG TTTTCCCTTA	2160
CCGGTTGGTT	
TTTCCACCAC CTTTTACATT TTCCTGGAAC ACTATACCCT CCCTCTTCAT	2220
TTGGCCCACC	

TCTAATTTTC	TTTCAGATCT	CCATGAAGAT	GTTACTTCCT	CCAGGAAGCC	TTATCTGACC	2280
CCTCCAAAGA	TGTCATGAGT	TCCTCTTTTC	ATTCTACTAA	TCACAGCATC	CATCACACCA	2340
TGTTGTGATT	ACTGATACTA	TTGTCTGTTT	CTCTGATTAG	GCAGTAAGCT	CAACAAGAGC	2400
TACATGGTGC	CTGTCTCTTG	TTGCTGATTA	TTCCCATCCA	AAAACAGTGC	CTGGAATGCA	2460
GACTTAACAT	TTTATTGAAT	GAATAAATAA	AACCCCATCT	ATCGAGTGCT	ACTTTGTGCA	2520
AGACCCGGTT	CTGAGGCATT	TATATTTATT	GATTTATTTA	ATTCTCATTT	AACCATGAAG	2580
GAGGTACTAT	CACTATCCTT	ATTTTATAGT	TGATAAAGAT	AAAGCCCAGA	GAAATGAATT	2640
AACTCACCCA	AAGTCATGTA	GCTAAGTGAC	AGGGCAAAAA	TTCAAACCAG	TTCCCCAACT	2700
TTACGTGATT	AATACTGTGC	TATACTGCCT	CTCTGATCAT	ATGGCATGGA	ATGCAGACAT	2760
CTGCTCCGTA	AGGCAGAATA	TGGAAGGAGA	TTGGAGGATG	ACACAAAACC	AGCATAATAT	2820
CAGAGGAAAA	GTCCAAACAG	GACCTGAACT	GATAGAAAAG	TTGTTACTCC	TGGTGTAGTC	2880
GCATCGACAT	CTTGATGAAC	TGGTGGCTGA	CACAACATAC	ATTGGCTTGA	TGTGTACATA	2940
TTATTTGTAG	TTGTGTGTGT	ATTTTATAT	ATATATTTGT	AATATTGAAA	TAGTCATAAT	3000
TTACTAAAGG	CCTACCATTT	GCCAGGCATT	TTTACATTTG	TCCCCTCTAA	TCTTTTGATG	3060
AGATGATCAG	ATTGGATTAC	TTGGCCTTGA	AGATGATATA	TCTACATCTA	TATCTATATC	3120
TATATCTATA	TCTATATCTA	TATCTATATC	TATATCTATA	TATGTATATC	AGAAAAGCTG	3180
AAATATGTTT	TGTAAAGTTA	TAAAGATTTC	AGACTTTATA	GAATCTGGGA	TTTGCCAAAT	3240
GTAACCCCTT	TCTCTACATT	AAACCCATGT	TGGAACAAAT	ACATTTATTA	TTCATTCATC	3300
AAATGTTGCT	GAGTCCTGGC	TATGAACCAG	ACACTGTGAA	AGCCTTTGGG	ATATTTTGCC	3360
CATGCTTGGG	CAAGCTTATA	TAGTTTGCTT	CATAAACTC	TATTTCAGTT	CTTCATAACT	3420
AATACTTCAT	GACTATTGCT	TTTCAGGTAT	TCCTTCATAA	CAAATACTTT	GGCTTTCATA	3480
TATTTGAGTA	AAGTCCCCCT	TGAGGAAGAG	TAGAAGAACT	GCACTTTGTA	AATACTATCC	3540
TGGAATCCAA	ACGGATAGAC	AAGGATGGTG	CTACCTCTTT	CTGGAGAGTA	CGTGAGCAAG	3600
GCCTGTTTTG	TTAACATGTT	CCTTAGGAGA	CAAACTTAG	GAGAGACACG	CATAGCAGAA	3660
AATGGACAAA	AACTAACAAA	TGAATGGGAA	TTGTACTTGA	TTAGCATTGA	AGACCTTGTT	3720
TATACTATGA	TAAATGTTTG	TATTTGCTGG	AAGTGCTACT	GACGGTAAAC	CCTTTTGT	3780
TAAATGTGTG	CCCTAGTAGC	TTGCAGTATG	ATCTATTTTT	TAAGTACTGT	ACTTAGCTTA	3840
TTTAAAAATT	TTATGTTTAA	AATTGCATAG	TGCTCTTTCA	TTGAAGAAGT	TTTGAGAGAG	3900

AGATAGAATT AAATTCACCTT ATCTTACCAT CTAGAGAAAC CCAATGTTAA AACTTTGTTG	3960
TCCATTATTT CTGTCTTTTA TTCAACATTT TTTTAGAGG GTGGGAGGAA TACAGAGGAG	4020
GTACAATGAT ACACAAATGA GAGCACTCTC CATGTATTGT TTTGTCCTGT TTTTCAGTTA	4080
ACAATATATT ATGAGCATAT TTCCATTTCA TTAAATATTC TTCCACAAAG TTATTTTGAT	4140
GGCTGTATAT CACCCTACTT TATGAATGTA CCATATTAAT TTATTTTCCTG GTGTGGGTTA	4200
TTTGATTTTA TAATCTTACC TTTAGAATAA TGAAACACCT GTGAAGCTTT AGAAAATACT	4260
GGTGCCTGGG TCTCAACTCC ACAGATTCTG ATTTAACTGG TCTGGGTAC AGACTAGGCA	4320
TTGGGAATTC AAAAAGTTCC CCCAGTGATT CTAATGTGTA GCCAAGATCG GGAACCCCTG	4380
TAGACAGGGA TGATAGGAGG TGAGCCACTC TTAGCATCCA TCATTTAGTA TTAACATCAT	4440
CATCTTGAGT TGCTAAGTGA ATGATGCACC TGACCCACTT TATAAAGACA CATGTGCAAA	4500
TAAAATTATT ATAGGACTTG GTTTATTAGG GCTTGTGCTC TAAGTTTCT ATGTTAAGCC	4560
ATACATCGCA TACTAAATAC TTTAAAATGT ACCTTATTGA CATACATATT AAGTGAAAAG	4620
TGTTTCTGAG CTAAACAATG ACAGCATAAT TATCAAGCAA TGATAATTTG AAATGAATTT	4680
ATTATTCTGC AACTTAGGGA CAAGTCATCT CTCTGAATTT TTTGTACTTT GAGAGTATTT	4740
GTTATATTTG CAAGATGAAG AGTCTGAATT GGTCAGACAA TGTCTTGTGT GCCTGGCATA	4800
TGATAGGCAT TTAATAGTTT TAAAGAATTA ATGTATTTAG ATGAATTGCA TACCAAATCT	4860
GCTGTCTTTT CTTTATGGCT TCATTAACTT AATTTGAGAG AAATTAATTA TTCTGCAACT	4920
TAGGGACAAG TCATGTCTTT GAATATTCTG TAGTTTGAGG AGAATATTTG TTATATTTGC	4980
AAAATAAAAT AAGTTTGCAA GTTTTTTTTT TCTGCCCCAA AGAGCTCTGT GTCCTTGAAC	5040
ATAAAATACA AATAACCGCT ATGCTGTAA TTATTGGCAA ATGTCCCAT TCAACCTAA	5100
GGAAATACCA TAAAGTAACA GATATACCAA CAAAAGGTTA CTAGTTAACA GGCATTGCCT	5160
GAAAAGAGTA TAAAGAATT TCAGCATGAT TTTCCATATT GTGCTTCCAC CACTGCCAAT	5220
AACA	5224

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGTCTTCAA GAATTCTCA

19

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTCAGTCAC CGGTGTCGGA

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCATTCTCTA GACACAGGTG

20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCGACACCG GTGACTGAAA

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCCACGGCC GCATTATATA C

21

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTATATAATG CGGCCGTGGG C

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCAGAAAATC CAGCAGGTAC C

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGACCGGTG CATTGCTGTG AACTCTGTA

29

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAAGTGGCC TGGATAAAGC TGAGTGG

27

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCACCGGTC TTTGTTATTG GCAGTGGT

28

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCCAGGCCA CTTATGAGCT CTGTGTCCTT

30

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TATCGGCCGG CATTGCTGTG AACTCT

26

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTACGGCCGC TTTGTTATTG GCAGTG

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCTTAATTA AAAGCAAACC TCACCTCCG

29

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGGAACAAA AGGTGATTAA AAAATCCCAG

30

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CACCTTTTGT TCCACCGCTC TGCTTATTAC

30

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCTTAATTA ACTGTGAAAG GTGGGAGC

28

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCAGCTCACT TAAGTTCATG TCG

23

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(A) NAME/KEY: CDS  
(B) LOCATION: 2..304

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

10

1	5	10	15
Ala Thr Gly Leu Thr Ser Ala Leu Asn Leu Pro Gln Val His Ala Phe			
20	25	30	
Val Asn Asp Trp Ala Ser Leu Asp Met Trp Trp Phe Ser Ile Ala Leu			
35	40	45	
Met Phe Val Cys Leu Ile Ile Met Trp Leu Ile Cys Cys Leu Lys Arg			
50	55	60	
Arg Arg Ala Arg Pro Pro Ile Tyr Arg Pro Ile Ile Val Leu Asn Pro			
65	70	75	80
His Asn Glu Lys Ile His Arg Leu Asp Gly Leu Lys Pro Cys Ser Leu			
85	90	95	
Leu Leu Gln Tyr Asp			
100			